

Fig. 1A

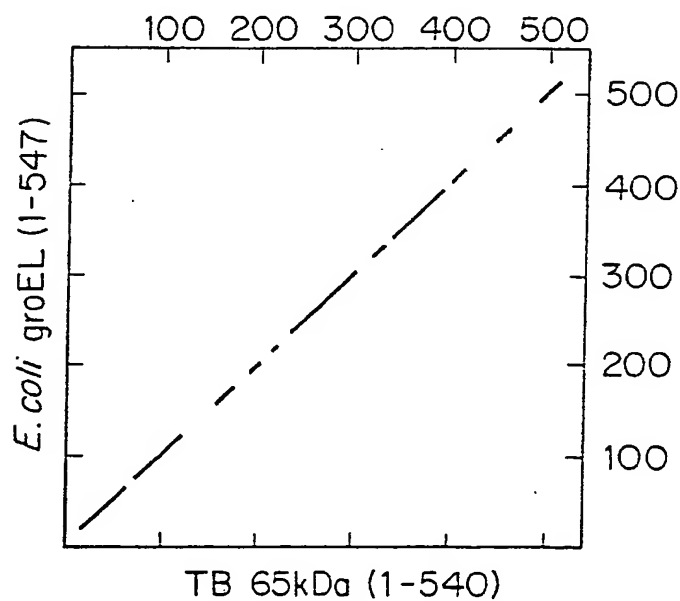
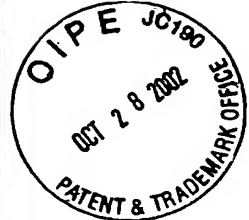


Fig. 1B



HUM1 1 10 20 30 40 50 60 70
MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVATMGPKGRTVIEQSWGS
GROEL -----MA-----AKDVKFGNDARVKMLRGVNVLADAVKVTGLGKGRNVVLDKSFCA

HUM1 71 80 90 100 110 120 130 140
PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTATVLAARSIKAGFEKISKGANPVEI
GROEL PTITKDGVSAREIEPEDKFENMGAMQMVKEVASKANDAAGDGTATVLAQAIIITEGLKAVAAGMNPMDL

HUM1 141 150 160 170 180 190 200 210
RRGVMLAVDAVIAELKKQSKPVTTPPEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGLNDE
GROEL KRGIDKAVTAAVEELKALSVPCSDSKAIAQVGTISANSDETGVKLLAEAMDVKVKEGVITVEDGTGLQDE

HUM1 211 220 230 240 250 260 270 280
LEIIEGMKFDGRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHKPLVILAEEDVDG
GROEL LDVVEGMQFDRGYLSFYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEG

HUM1 281 290 300 310 320 330 340 350
EALSTLVNRLKVLQVAVKAPGFGDNRKNQLKDMAIATGGAVFGEGLTLNLEDVQPHDLGKVGEVIV
GROEL EALATAVVNTIRGIVKVAAPGFGDRRKAMLQDIATLTGCTVISEE-IGMELEKATLEDLGQAKRVVI

HUM1 351 360 370 380 390 400 410 420
TKDDAMLLKGGDKAQIEKRIQIEIEQLDVTTSEYEKEKLNRLAKLSDGVAVLVKVGTSDEVNEKKDR
GROEL NKDTTTIIDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKAR

Figure 2A



421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGALLRCIPALD	SLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLI					
	:	:	:	:	:	:	:
GROEL	VEDALHATRAAVEEGVAGGVALIRVASKLADLRGQ	NEDQNVVSSSL-RAMEAPLRQIVLNCGEPSVV					
491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSEVGYDAMAGDFVNMVEKGIIDPTKV	VVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA					
	:	:	:	:	:	:	:
GROEL	ANTVKGGDGNYGYNAAATEEYGNMIDMGILDPTK	VTRSALQYAAASVAGLMITTECMVTDLPKND-AADLGA					
561	570						
HUMP1	MGGMGG--GMGGGNF						
	:	:	:	:	:	:	:
GROEL	AGGMGGMGGMGGNM-						

Total score = 4667, 5 breaks
276 identities out of 545 possible matches between residues

25 random runs
Alignment score = 65.34 SD Standard deviation = 18.94 Mean = 3429.48

Figure 2B



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	1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRLAPHLTRAYAKDVKFGADARALMLQGVDDLADAVAVTMGPKGRTVIIEQSWGS							
ML65K	M-----AKTIAYDEEARGLERGLNSLADAVKVTLGPKGRNVVLEKKWGA							
	71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLSIAKEGFEKISKGANPVEI							
ML65K	PTITNDGVSIAKEIELEDPEYKIGAEVLVKEVAKKTDVAGDGTTTATVLAQALVKEGLRNVAAGANPLGL							
	141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVTIVKDGKTLNDE							
ML65K	KRGIEKAVDKVTETLLKDAKEVETKEQIAATAAISAGDQSIGDLIAEAMDKVGNEGVTIVEESNTFGLQ							
	211	220	230	240	250	260	270	280
HUMP1	LEIEGMKFDGRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHKPLVIAEDVDG							
ML65K	LELTEGMRFDKGYISGYFVTDARERQEAQVLEEPYILLVSSKVSTVKDPLPLEKVIQAGKSLIIAEDVEG							
	281	290	300	310	320	330	340	350
HUMP1	EALSTLVNRLKVLQVAVKAPGFGDNRRKNQLKDMAIATGGAVFGEGLTNLEDVQPHDLGKVGIV							
ML65K	EALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMAILTGAQVISEE-VGLTLENTDLSLLGKARKVVM							
	351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKGKDKAQIEKRIQEIIEQLDVTTSYEKEKLNERLAKLSDGAVLVKVGTSDEVNEKKDR							
ML65K	TKDETTIVEGAGDTDAIAGRVAQIRTEIENSDDSDYDREKLQERLAKLAGVAVIKAGAATEVELKERKHR							

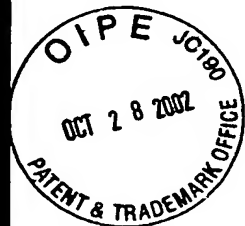
Figure 3A



421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLI						
ML65K	IEDAVRNAKAAVEEGIVAGGGVTLQAAPALDKLKLTCDEAT-GANIVKVALEAPLKQIAFNSGMEPGVV						
491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA						
ML65K	AEKVRNLSVGHGLNAATGEYEDLLKAGVADPVKVTRSAQNAAAGLFTT-EAVVADKPEKTAAPASDP						
561	570						
HUMP1	MGGMGGMGGGMF						
ML65K	TGGMGG-MD---F						

Total score = 4552, 7 breaks
255 identities out of 540 possible matches between residues
25 random runs
Alignment score = 47.73 SD Standard deviation = 23.86 Mean = 3413.16

Figure 3B



1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVATMGPKGRTVIIIEQSWGS						
TB65K	M-----AKTIAYDEEARGLERGLNALADAVKVTLGPKGRNVVLEKKWGA						
71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTATATVLARSIAKEGFEKISKGANPVEI						
TB65K	PTITNDGVSIAKEIELEDPEYKIGAEVLVEVAKKTDVAGDGTATATVLAQALRKEGLRNVAAGANPLGL						
141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVTIVKDGKTLNDE						
TB65K	KRGIEKAVEKVTETLLKGAKAEVETKEQIAATAAISA-GDQSIGDLIAEAMDKVGNEGVITVEESNTFFGLQ						
211	220	230	240	250	260	270	280
HUMP1	LEIIIEGKMFDRGYISPYFINTSKGQKCEFDQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIAEDVDG						
TB65K	LELTEGMRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKDLLPLEKVGAGKPLLIIEAEDVEG						
281	290	300	310	320	330	340	350
HUMP1	EALSTLVNRLKVLQVVAVKAPGFGDNRNKQKDMAIATGGAVFGEGLTNLEDDVQPHDLGKVGIV						
TB65K	EALSTLVVNKIRGTGTFKSVAVKAPGFGDRRKAMLQDMAILTGGQVISEE-VGLTLENADLSLLGKARKVVV						
351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKGGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGTSDEVNEKKDR						
TB65K	TKDETTIVEGAGDTDAIAGRVAQIRQEIENSDDYDREKLQERLAKLAGGVAVIKAGAAATEVELKERKHR						

Figure 4A

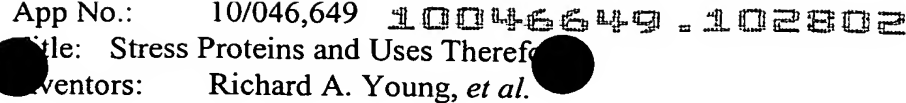


Figure 4B

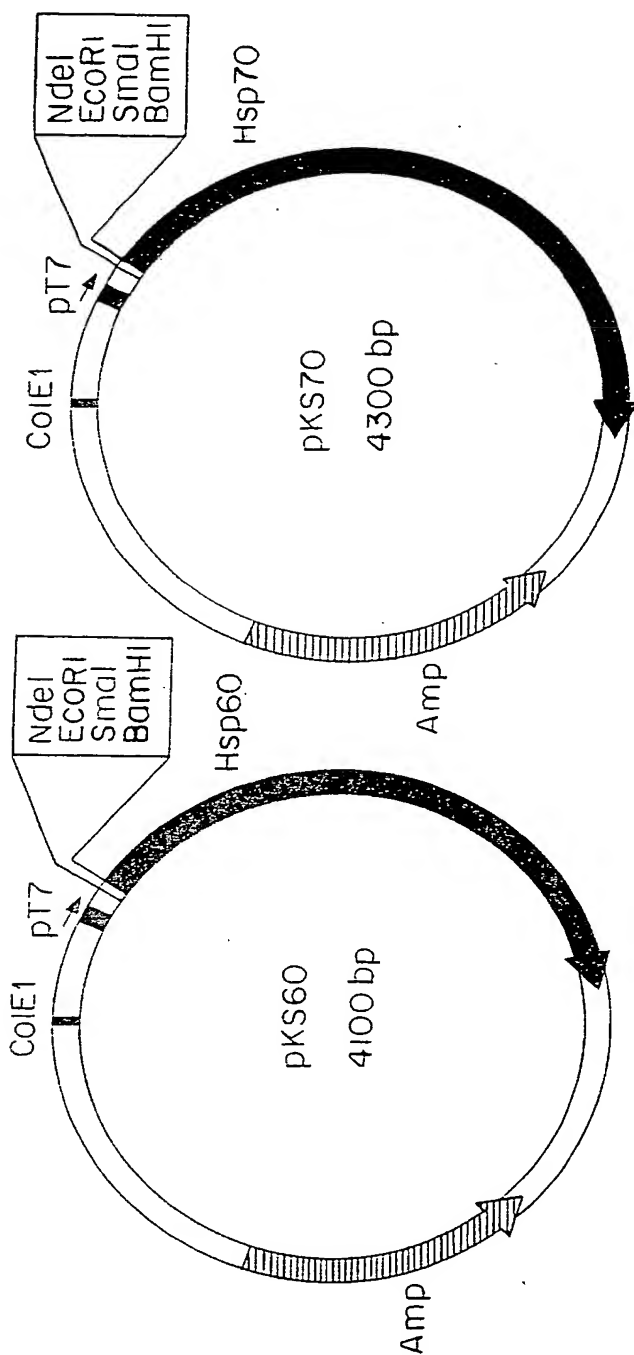


FIG. 5

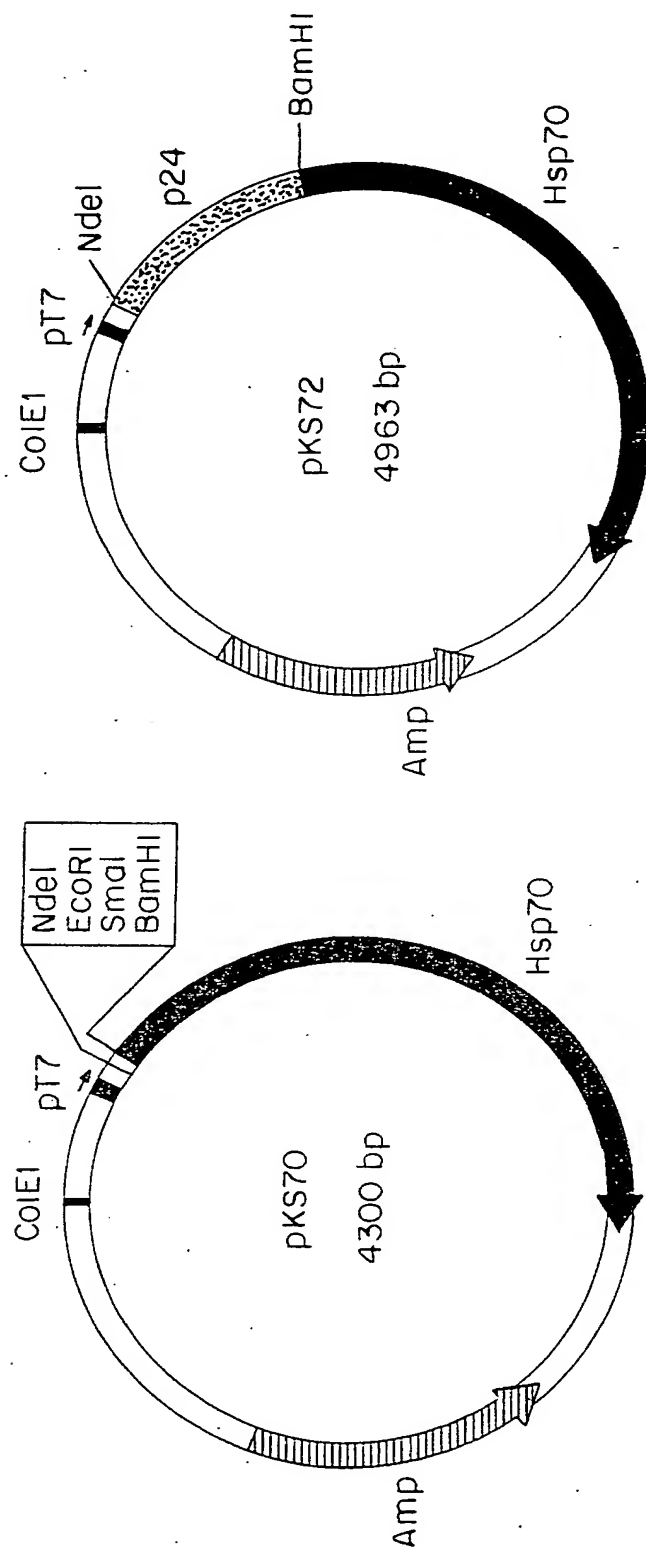


FIG. 6



App No.: 10/046,649
Title: Stress Proteins and Uses Therefor
Inventors: Richard A. Young, et al.

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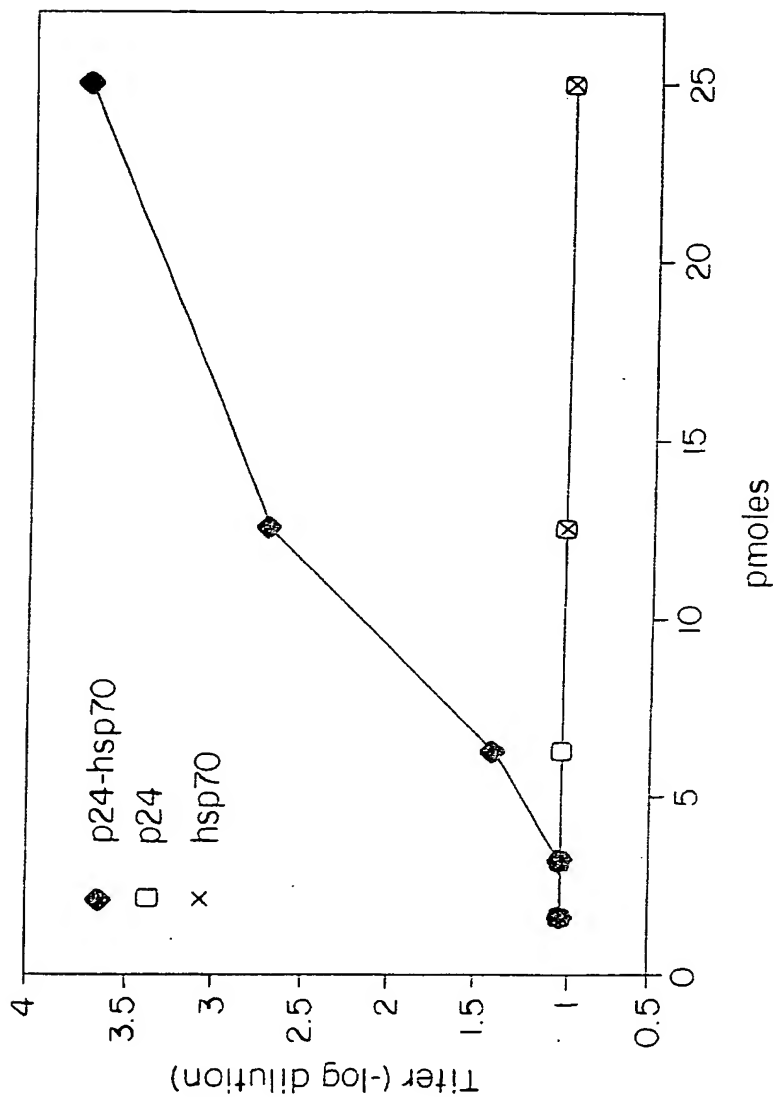


FIG. 7